

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

5           (i) APPLICANT:  
              (A) NAME: Max-Planck-Gesellschaft zur Foerderung  
                          der  
                          Wissenschaften e.v.  
0           (B) STREET: Hofgartenstrasse 2  
              (C) CITY: Muenchen  
              (E) COUNTRY: Germany  
              (F) POSTAL CODE (ZIP): 80539

(ii) TITLE OF INVENTION: Tuberculosis vaccine

(iii) NUMBER OF SEQUENCES: 2

20 (iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25 (2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1881 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ix) FEATURE:  
      (A) NAME/KEY: CDS  
      (B) LOCATION: 1..1878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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40      ATG ACA GAC GTG AGC CGA AAG ATT CGA GCT TGG GGA CGC CGA TTG ATG
Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met
          1       5       10      15

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45 ATC GGC ACG GCA GCG GCT GTA GTC CTT CCG GGC CTG GTG GGG CTT GCC  
 Ile Gly Thr Ala Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala  
           20                 25                 30

GGC GGA GCG GCA ACC GCG GGC GCG TTC TCC CGG CCG GGG CTG CCG GTC  
 Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro. Gly Leu Pro Val  
 50 35 40 45

GAG TAC CTG CAG TCT GCA AAG CAA TCC GCT GCA AAT AAA TTG CAC TCA  
 Glu Tyr Leu Gln.Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser  
 50 55 60

35 GCA GGA CAA AGC ACG AAA GAT GCA TCT GCA TTC AAT AAA GAA AAT TCA 240  
Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser  
65 70 75 80

60	ATT TCA TCC ATG GCA CCA CCA GCA TCT CCG CCT GCA AGT CCT AAG ACG	288
	Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr	
	85                    90                    95	

	CCA ATC GAA AAG AAA CAC GCG GAT GAA ATC GAT AAG TAT ATA CAA GGA Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly 100 105 110	336
5	TTG GAT TAC AAT AAA AAC AAT GTA TTA GTA TAC CAC GGA GAT GCA GTG Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val 115 120 125	384
10	ACA AAT GTG CCG CCA AGA AAA GGT TAC AAA GAT GGA AAT GAA TAT ATT Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile 130 135 140	432
15	GTT GTG GAG AAA AAG AAG AAA TCC ATC AAT CAA AAT ATT GCA GAC ATT Val Val Glu Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile 145 150 155 160	480
20	CAA GTT GTG AAT GCA ATT TCG AGC CTA ACC TAT CCA GGT GCT CTC GTA Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val 165 170 175	528
25	AAA GCG AAT TCG GAA TTA GTA GAA AAT CAA CCA GAT GTT CTC CCT GTA Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val 180 185 190	576
30	AAA CGT GAT TCA TTA ACA CTC AGC ATT GAT TTG CCA GGT ATG ACT AAT Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn 195 200 205	624
35	CAA GAC AAT AAA ATC GTT GTA AAA AAT GCC ACT AAA TCA AAC GTT AAC Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn 210 215 220	672
40	AAC GCA GTA AAT ACA TTA GTG GAA AGA TGG AAT GAA AAA TAT GCT CAA Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln 225 230 235 240	720
45	GCT TAT CCA AAT GTA AGT GCA AAA ATT GAT TAT GAT GAC GAA ATG GCT Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala 245 250 255	768
50	TAC AGT GAA TCA CAA TTA ATT GCG AAA TTT GGT ACA GCA TTT AAA GCT Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala 260 265 270	816
55	GTA AAT AAT AGC TTG AAT GTA AAC TTC GGC GCA ATC AGT GAA GGG AAA Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys 275 280 285	864
60	ATG CAA GAA GAA GTC ATT AGT TTT AAA CAA ATT TAC TAT AAC GTG AAT Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn 290 295 300	912
65	GTT AAT GAA CCT ACA AGA CCT TCC AGA TTT TTC GGC AAA GCT GTT ACT Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr 305 310 315 320	960
70	AAA GAG CAG TTG CAA GCG CTT GGA GTG AAT GCA GAA AAT CCT CCT GCA Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala 325 330 335	1008
	TAT ATC TCA AGT GTG GCG TAT GGC CGT CAA GTT TAT TTG AAA TTA TCA Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser 340 345 350	1056
	ACT AAT TCC CAT AGT ACT AAA GTA AAA GCT GCT TTT GAT GCT GCC GTA Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val 355 360 365	1104
	AGC GGA AAA TCT GTC TCA GGT GAT GTA GAA CTA ACA AAT ATC ATC AAA Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys 370 375 380	1152

	AAT TCT TCC TTC AAA GCC GTC ATT TAC GGA GGT TCC GCA AAA GAT GAA Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu 385 390 395 400	1200
5	GTT CAA ATC ATC GAC GGC AAC CTC GGA GAC TTA CGC GAT ATT TTG AAA Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys 405 410 415	1248
10	AAA GGC GCT ACT TTT AAT CGA GAA ACA CCA GGA GTT CCC ATT GCT TAT Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr 420 425 430	1296
15	ACA ACA AAC TTC CTA AAA GAC AAT GAA TTA GCT GTT ATT AAA AAC AAC Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn 435 440 445	1344
20	TCA GAA TAT ATT GAA ACA ACT TCA AAA GCT TAT ACA GAT GGA AAA ATT Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile 450 455 460	1392
25	AAC ATC GAT CAC TCT GGA GGA TAC GTT GCT CAA TTC AAC ATT TCT TGG Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp 465 470 475 480	1440
30	GAT GAA GTA AAT TAT GAT CCT GAA GGT AAC GAA ATT GTT CAA CAT AAA Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys 485 490 495	1488
35	AAC TGG AGC GAA AAC AAT AAA AGC AAG CTA GCT CAT TTC ACA TCG TCC Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser 500 505 510	1536
40	ATC TAT TTG CCA GGT AAC GCG AGA AAT ATT AAT GTT TAC GCT AAA GAA Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu 515 520 525	1584
45	TGC ACT GGT TTA GCT TGG GAA TGG TGG AGA ACG GTA ATT GAT GAC CGG Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg 530 535 540	1632
50	AAC TTA CCA CTT GTG AAA AAT AGA AAT ATC TCC ATC TGG GGC ACC ACG Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr 545 550 555 560	1680
55	CTT TAT CCG AAA TAT AGT AAT AAA GTA GAT AAT CCA ATC GAA TAT GCA Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala 565 570 575	1728
60	TTA GCC TAT GGA AGT CAG GGT GAT CTT AAT CCA TTA ATT AAT GAA ATC Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile 580 585 590	1776
65	AGC AAA ATC ATT TCA GCT GCA GTT CTT TCC TCT TTA ACA TCG AAG CTA Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu 595 600 605	1824
70	CCT GCA GAG TTC GTT AGG CGC GGA TCC GGA ATT CGA AGC TTA TCG ATG Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met 610 615 620	1872
75	TCG ACG TAG Ser Thr 625	1881

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 626 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10 Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met  
1 5 10 15

15 Ile Gly Thr Ala Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala  
20 25 30

Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val  
35 40 45

20 Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser  
50 55 60

Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser  
65 70 75 80

25 Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr  
85 90 95

Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly  
30 100 105 110

Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val  
115 120 125

35 Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile  
130 135 140

Val Val Glu Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile  
40 145 150 155 160

Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val  
165 170 175

45 Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val  
180 185 190

Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn  
50 195 200 205

55 Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn  
210 215 220

Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln  
225 230 235 240

Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala  
245 250 255

60 Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala  
260 265 270

Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys  
275 280 285

65 Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn  
290 295 300

Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr  
70 305 310 315 320

Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala  
325 330 335

Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser  
340 345 350  
5 Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val  
355 360 365  
Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys  
370 375 380  
10 Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu  
385 390 395 400  
Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys  
405 410 415  
15 Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr  
420 425 430  
20 Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn  
435 440 445  
Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile  
450 455 460  
25 Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp  
465 470 475 480  
Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys  
485 490 495  
30 Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser  
500 505 510  
Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu  
515 520 525  
35 Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg  
530 535 540  
40 Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr  
545 550 555 560  
Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala  
565 570 575  
45 Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile  
580 585 590  
50 Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu  
595 600 605  
Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met  
610 615 620  
55 Ser Thr  
625